CRF Prors Corrected by the STIC	Systems Branch / /
Number: 08/249,671	CRF Processing Date: 66/6/94 Edited by:
Changed a file from non-ASCII to ASCII	Verified by: (STIC s
Changed the margins in cases where the sequence text was "	wrapped" down to the next line
Edited a format error in the Current Application Data section, s	specifically:
Edited the Current Application Data section with the actual current applicant was the prior application data; or other	rent number. The number inputted by the
Added the mandatory heading and subheadings for "Current A	Application Data".
Edited the "Number of Sequences" field. The applicant spelled	d out a number instead of using an integer.
Changed the spelling of a mandatory field (the headings or sub-	oheadings), specifically:
Inserted a space between the last nucleic designator and the n	nucleic number for sequences:
Deleted page numbers in the text of the sequence listing, which	h is considered invalid text.
Corrected the SEQ ID NO when obviously incorrect. The sequ	ence numbers that were edited were:
Inserted a nucleic number at the end of a nucleic line. SEQ ID) NO's edited:
Corrected subheading placement. All responses must be on the applicant placed a response below the subheading, this was m	ne same line as each subheading. If the noved to its appropriate place.
Inserted colons after headings/subheadings. Headings edited	included:
Deleted extra, invalid, headings used by an applicant, specifica	ally:
Deleted non-ASCII "garbage" at the end of files, and other inv	valid text, such as a secretary's initials.
Inserted mandatory headings, specifically:	
Corrected an obvious error in the response, specifically:	
Edited identifiers where upper case is used but lower case is	required, or vice versa.
Corrected an error in the Number of Sequences field, specifica	ally:
A "Hard Page Break" code was inserted by the applicant. All of	occurrences had to be deleted.
Other: Startes applicant now	mes on same lin

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

8/01/93

RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671

DATE: 06/16/94 TIME: 16:58:10

INPUT SET: S2395.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

```
1
                                       SEQUENCE LISTING
 2
 3
     (1)
           General Information:
                                                                ENTERE
 4
 5
          (i) APPLICANTS:
                               Hauptmann, R.
 6
                               Falkner, E.
 7
                               Bodo, G.
 8
                               VoÃ, T.
 9
                               Maurer- Fogy, I.
10
         (ii) TITLE OF INVENTION:
                                   Process for Preparing and Purifying
11
12
                                    alpha-Interferon
13
14
        (iii) NUMBER OF SEQUENCES: 12
15
16
         (iv) CORRESPONDENCE ADDRESS:
               (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox
17
               (B) STREET: 1100 New York Avenue, Suite 600
18
               (C) CITY: Washington
19
20
               (D) STATE: D.C.
21
               (E) COUNTRY: U.S.A.
               (F) ZIP: 20005
22
23
24
          (v) COMPUTER READABLE FORM:
               (A) MEDIUM TYPE: Floppy disk
25
               (B) COMPUTER: IBM PC compatible
26
               (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27
               (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
28
29
         (vi) CURRENT APPLICATION DATA:
30
               (A) APPLICATION NUMBER:
31
32
               (B) FILING DATE: herewith
33
               (C) CLASSIFICATION:
34
       (viii) ATTORNEY/AGENT INFORMATION:
35
               (A) NAME: Esmond, Robert W. RWE/EG
36
               (B) REGISTRATION NUMBER: 32,893
37
               (C) REFERENCE/DOCKET NUMBER: 0652.1350000
38
39
40
         (ix) TELECOMMUNICATION INFORMATION:
41
               (A) TELEPHONE: (202) 371-2600
               (B) TELEFAX: (202) 371-2540
42
43
44
45
     (2) INFORMATION FOR SEQ ID NO: 1:
46
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671

DATE: 06/16/94 TIME: 16:58:15

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47
48
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49
               (A) LENGTH: 25 base pairs
50
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: both
51
52
               (D) TOPOLOGY: unknown
53
         (ii) MOLECULE TYPE: cDNA
54
55
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
56
57
58
    CGTCTTCAAG AATTCGAGAT TATCG
                                                                              25
59
     (2) INFORMATION FOR SEQ ID NO: 2:
60
61
62
          (i) SEQUENCE CHARACTERISTICS:
63
               (A) LENGTH: 56 base pairs
64
               (B) TYPE: nucleic acid
65
               (C) STRANDEDNESS: both
66
               (D) TOPOLOGY: unknown
67
        (ii) MOLECULE TYPE: cDNA
68
69
70
71
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
72
73
74
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                                                                             56
75
76
    (2) INFORMATION FOR SEQ ID NO: 3:
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78
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               (B) TYPE: nucleic acid
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81
               (C) STRANDEDNESS: both
               (D) TOPOLOGY: unknown
83
84
        (ii) MOLECULE TYPE: cDNA
85
86
87
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
88
89
                                                                              35
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91
92
    (2) INFORMATION FOR SEO ID NO: 4:
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94
          (i) SEQUENCE CHARACTERISTICS:
95
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96
               (C) STRANDEDNESS: both
97
               (D) TOPOLOGY: unknown
98
99
```

RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671

DATE: 06/16/94 TIME: 16:58:21

34

INPUT	SET:	S2395.raw

													IN	PUT S	SET: S	52395.raw
100	(ii)	MOL	ECUL	E TY	PE:	cDNA										
101																
102																
103	/ \	0.00	TTT3.TC		0 OD T	DE T 01		TO T								
104	(X1)	SEQ	UENC.	E DE	SCRI.	P.I.TO	N: S.	EQ I	טא ט	: 4:						
105 106	GGCAGATO	יארי א	ייים בי אי	ת א כי כי <i>ו</i>	יידי א	rmem.	אכיכיא	א ידי א	~							
107	GGCAGATC	AC A	IGCA	IAGG	C AI	1161	AJUA	MIM	J							
108	(2) INFO	RMAT	TON	FOR :	SEO :	א מד	7									
109	(2) 1111	, ICI II I I	1011	. 010	JLQ .	10 11	J. J	•								
110	(i)	SEQ	UENC	E CH	ARAC'	reri:	STIC	S:								
111		-) LE						s							
112		(в) TY	PE: a	amino	o ac	id									
113		(D) TO	POLO	GY:	line	ar									
114																
115	(ii)	MOL	ECUL:	E TY	PE:]	prote	ein									
116																
117																
118																
119	(xi)	SEQ	UENC:	E DE	SCRI	PTIO	N: S	EQ I	ои о	: 5:						
120		_		_				_			_	_				
121	_	Asp	Leu	Pro		Thr	His	Ser	Leu		Ser	Arg	Arg	Thr		Met
122	1				5					10					15	
123	7	. .	7. 7	~1	3.6 - L	7	7	- 1.	~	T	Dla a		~	T	T	3
124	Let	Leu	Ата		мет	Arg	Arg	тте		ьeu	Pne	ser	Cys		ьys	Asp
125 126				20					25					30		
127	Λrc	Arg	λαn	Dhe	Glv	Dhe	Dro	Gln	Glu	Glu	Dhe	Gl v	λan	Gln	Dhe	Gln
128	AI 9	ng	35	FIIC	Gry	LIIC	110	40	GIU	GIU	1 110	O±y	45	0111	1110	QIII
129			33													
130	Lvs	Ala	Glu	Thr	Ile	Pro	Val	Leu	His	Glu	Met	Ile	Gln	Gln	Ile	Phe
131	-1-	50					55					60				
132																
133	Asn	Leu	Phe	Ser	Thr	Lys	Asp	Ser	Ser	Ala	Ala	Trp	Asp	Glu	Thr	Leu
134	65					70	_				75	_	_			80
135																
136	Let	. Asp	Lys	Phe	Tyr	Thr	Glu	Leu	Tyr	Gln	Gln	Leu	Asn	Asp	Leu	Glu
137					85					90					95	
138				_		_	_		_	_	_					
139	Ala	Cys	Val		Gln	Gly	Val	Gly		Thr	Glu	Thr	Pro	Leu	Met	Lys
140	•			100					105					110		
141	6 1.	.	a	- 1 -	.	77-	**- 7	7	T		D1	~ 1	7	- 1 -	m1	T
142	GIU	Asp		шe	Leu	Ата	vaı		ьуs	Tyr	Pne	GIN		шe	Thr	Leu
143			115					120					125			
144	Π1 22	Leu	Tara	C1.,	Tarc	Tazo	Тугъ	Car	Dro	Cvc	Nla	Trn	Glu	Val	₩-1	7) rcr
145 146	1 7 1	130	_	GIU	пуъ	пåр	135	261	PIO	Cys	нта	140	GIU	vaı	vai	AIG
147		130					133					140				
148	בומ	Glu	Tle	Met	Ara	Ser	Phe	Ser	Leu	Ser	Thr	Asn	Leu	Gln	Glu	Ser
149	145				9	150		~~_	u	~~_	155					160
150																
151	Lev	Arg	Ser	Lys	Glu											
152		_		-	165											

RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671

DATE: 06/16/94 TIME: 16:58:27

													II	VPUT	SET:	S2395.ra
153 154 155	(2)	INF	ORMA'	TION	FOR	SEQ	ID 1	NO:	6:							
156 157 158 159 160 161		(i	(. (: (:	QUENGA) Li B) T C) S D) T	ENGTI YPE : FRANI	H: 4: nuc: DEDN	95 ba leic ESS:	ase j acio botl	pair: d	S						
162 163		(ii) MO:	LECU	LE T	YPE:	cDN	A								
164 165 166 167 168		(ix	()	ATURI A) N B) L	AME/I			495								
169 170		(xi) SE	QUEN	CE DI	ESCR:	IPTI	ON: S	SEQ :	ID N	D: 6	:				
171 172 173 174		GAT Asp														48
175 176 177 178 179		CTG Leu														96
180 181 182 183		CGT Arg													CAA Gln	144
184 185 186 187		GCT Ala 50														192
188 189 190 191		CTC Leu														240
192 193 194 195		GAC Asp														288
196 197 198 199		TGT Cys														336
200 201 202 203		GAC Asp														384
204 205		CTG Leu														432

RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671

DATE: 06/16/94 TIME: 16:58:32

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206		130					135					140					
207	~~-	~															
208					AGA												480
209		GIu	тте	Met	Arg		Pne	Ser	Leu	Ser		Asn	Leu	GIn	Glu		
210	145					150					155					160	
211																	
212				AAG													495
213	Leu	Arg	Ser	Lys													
214					165												
215																	
216																	
217	(2)	INF	ORMA'	rion	FOR	SEQ	ID 1	. OV.	7:								
218																	
219					ENCE												
220			()	A) LI	ENGT	H: 16	55 ar	mino	acio	ds							
221			(1	3) T	YPE:	amir	no a	cid									
222			(1) T(OPOL	OGY:	line	ear									
223																	
224		(ii)	MO	LECUI	LE T	YPE:	prot	tein									
225																	
226		(xi)	SE	QUEN	CE DI	ESCR:	IPTI	: NC	SEQ :	ID NO	0: 7	:					
227																	
228	Cys	Asp	Leu	Pro	Gln	Thr	His	Ser	Leu	Gly	Ser	Arg	Arg	Thr	Leu	Met	
229	1	_			5					10			_		15		
230																	
231	Leu	Leu	Ala	Gln	Met	Arq	Arq	Ile	Ser	Leu	Phe	Ser	Cys	Leu	Lys	Asp	
232				20		-			25				•	30	•	•	
233																	
234	Ara	Arq	Asp	Phe	Gly	Phe	Pro	Gln	Glu	Glu	Phe	Gly	Asn	Gln	Phe	Gln	
235	3	5	35		1			40					45				
236																	
237	Lvs	Ala	Glu	Thr	Ile	Pro	Val	Leu	His	Glu	Met	Ile	Gln	Gln	Ile	Phe	
238	-1	50					55					60					
239																	
240	Asn	Leu	Phe	Ser	Thr	Lvs	Asp	Ser	Ser	Ala	Ala	Tro	Asp	Glu	Thr	Leu	
241	65			501		70					75					80	
242	0.5										, ,						
243	T.e.	Asp	Lvs	Phe	Tyr	Thr	Glu	Leu	Tvr	Gln	Gln	T.eu	Asn	Asp	Leu	Glu	
244	204	1101	-1-		85				- 1 -	90					95		
245					0.5												
246	Δla	Cvs	Val	Tle	Gln	Glv	Val	Glv	Val	Thr	Glu	Thr	Pro	Len	Met	Tvs	
247		O _I S	• • • •	100	02	O-1		0-1	105					110		_1.	
248																	
249	Glu	Agn	Ser	Tle	Leu	Δla	Val	Δra	Lvg	ጥህድ	Dhe	Gln	Δrα	Tle	Thr	T.eu	
250	Giu	App	115	110	пси	пта	Val	120	цуБ	ı yı	FIIC	OIII	125	110	1111	ЦСИ	
250 251			113					120					123				
252	ጥ፣ ፣ •	Leur	Larg	C1 11	Lys	Larg	Тугъ	Ser	Dro	Cve	Δla	Trn	G111	Va 1	Va 1	Δra	
252 253	тАт	130	пys	GIU	пур	пур	135	OCT	FIO	Cys	ліа	140	GIU	Val	Val	A. 9	
253 254		130					133					740					
25 4 255	ה ד מ	۲۱۰۰	T1 ^	Mo+	Arg	Ser.	Dha	Sar	T. 211	Sar	Thr	Δan	T,211	Gln	Glu	Ser	
255 256		GIU	116	rie C	nr 9	150	FIIG	DOT	Leu	DCI	155	L'OII	шeu	O 1 1 1	JIU	160	
256 257	145					100					100					100	
	Len	λνα	802	Tare	G1												
258	пeп	Arg	261	Lys	GIU												

RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671

DATE: 06/16/94 TIME: 16:58:38

INPUT SET: S2395.raw

***** PREVIOUSLY ERRORED SEQUENCES - EDITED *****

60	(2) INFORMATION FOR SEQ ID NO: 2:
61	
62	(i) SEQUENCE CHARACTERISTICS:
63	(A) LENGTH: 56 base pairs
64	(B) TYPE: nucleic acid
65	(C) STRANDEDNESS: both
66	(D) TOPOLOGY: unknown
67	(22) MOVERSTER TOWNS DATA
68	(ii) MOLECULE TYPE: cDNA
69 70	
70 71	
71 72	() GROVENCE DECORIDATION, CEO ID NO. 2
72 73	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
73 74	GACTTCAGAA GCTTCTGCAG TTACGATCGT TATCATTCCT TACTTCTTAA ACTTTC 56
75	GACIICAGAA GCIICIGCAG IIACGAICGI IAICAIICCI IACIICIIAA ACIIIC
75	
154	(2) INFORMATION FOR SEQ ID NO: 6:
155	
156	(i) SEQUENCE CHARACTERISTICS:
157	(A) LENGTH: 495 base pairs
158	(B) TYPE: nucleic acid
159	(C) STRANDEDNESS: both
160	(D) TOPOLOGY: unknown
161	
162	(ii) MOLECULE TYPE: cDNA
163	
164	
165	(ix) FEATURE:
166	(A) NAME/KEY: CDS
167	(B) LOCATION: 1495
168	
169	
170	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
171	
172	TGT GAT CTG CCT CAA ACC CAC AGC CTG GGT AGC AGG AGG ACC TTG ATG 48
173	Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
174	1 5 10 15
175	CTC CTG GCA CAG ATG AGG AGA ATC TCT CTT TTC TCC TGC TTG AAG GAC 96
176	C10 C10 CCA C10 1110 1100 1101 1110 101 C11 110 100 10
177	Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
178	20 25 30
179	AGA CGT GAC TTT GGA TTT CCC CAG GAG GAG TTT GGC AAC CAG TTC CAA 144
180	AGA CGT GAC TTT GGA TTT CCC CAG GAG GAG TTT GGC AAC CAG TTC CAA 144 Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
181 182	35 40 45
182	22 40 40
103	

RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671

DATE: 06/16/94 TIME: 16:58:43

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:	186	_	50					55					60						
:	187																		
:	188	AAT	CTC	TTC	AGC	ACA	AAG	GAC	TCA	TCT	GCT	GCT	TGG	GAT	GAG	ACC	CTC	240	
	189	Asn	Leu	Phe	Ser	Thr	Lvs	Asp	Ser	Ser	Ala	Ala	Tro	Asp	Glu	Thr	Leu		
	190	65					70	_				75					80		
	191											_							
	192	CTA	GAC	AAA	TTC	TAC	ACT	GAA	CTC	TAC	CAG	CAG	CTG	AAT	GAC	CTG	GAA	288	
	193				Phe														
	194		•	-		85				-	90					95			
	195																		
	196	GCC	TGT	GTG	ATA	CAG	GGG	GTG	GGG	GTG	ACA	GAG	АСТ	CCC	CTG	ATG	AAG	336	
	197				Ile														
	198		- 1		100		2		2	105					110		-2-		
	199																		
	200	GAG	GAC	TCC	ATT	CTG	GCT	GTG	AGG	AAA	TAC	TTC	CAA	AGA	ATC	ACT	CTC	384	
	201				Ile														
	202			115					120	-1-	-1-			125					
	203																		
	204	TAT	CTG	AAA	GAG	AAG	AAA	TAC	AGC	CCT	TGT	GCC	TGG	GAG	GTT	GTC	AGA	432	
- 2	205				Glu														
	206	-	130	-		•	•	135					140				5		
	207																		
2	208	GCA	GAA	ATC	ATG	AGA	TCT	TTT	TCT	TTG	TCA	ACA	AAC	TTG	CAA	GAA	AGT	480	
2	209	Ala	Glu	Ile	Met	Arg	Ser	Phe	Ser	Leu	Ser	Thr	Asn	Leu	Gln	Glu	Ser		
2	210	145					150					155					160		
2	211																		
2	212	TTA	AGA	AGT	AAG	GAA												495	
	213	Leu	Arg	Ser	Lys														
	214					165													
	215																		
4	216																		
	261	(2)	INFO	DRMAT	TION	FOR	SEO	ID N	TO: 8	3 :									
	262																		
2	263		(i)	SEC	UENC	CE CH	IARAC	TER	STIC	CS:									
2	264			(1	A) LE	ENGTH	I: 86	9 ba	se p	airs	3								
2	265			(E	3) TY	PE:	nucl	eic	acio	ì									
2	266			((C) S7	RANI	DEDNE	ESS:	both	ı									
2	267			(I) TC	POLC	GY:	unkr	nown										
2	268																		
2	269		(ii)	MOI	LECUI	E TY	PE:	CDNA	7										
2	270																		
	271																		
	272																		
	273		(xi)	SEÇ	OUENC	E DE	ESCRI	PTIC	N: 5	SEQ I	D NO): 8:							
	274						. 							. 				~	
	275	GAAT	TCG	AGA T	TATC	GTC	AC TO	CAAT	GCT'	. CGC	CAATA	ATGG	CGCA	'AAA	'GA (CAAC	CAGCG	G 60)
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	278 279	CNCC	ኋ አ ጥ አ ረ	יים יי	עברייי	ישער	ים מי	ייייי אַ יַ	الرئسة	\	<u> </u>	רולוי /ל ולניין	ע ע טיטיי	עמטיי	הככ ה	יריייי	CAGTA	A 180	1
4	۷/3	GACC	HIH	A DOL	2GC 1 C		ال قال	25T T.F	Y G I F	· AAC	THAM.	THI	TAFF	JUCH.			ALDM.	Y 19(,

RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671

DATE: 06/16/94 TIME: 16:58:49

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280 281 282	AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA TAGTCGCTTT	240
282 283 284	GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTTATGAA AAAGAATATC	300
285 286	GCATTTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAATGCCTA TGCATGTGAT	360
287 288	CTGCCTCAAA CCCACAGCCT GGGTAGCAGG AGGACCTTGA TGCTCCTGGC ACAGATGAGG	420
289 290	AGAATCTCTC TTTTCTCCTG CTTGAAGGAC AGACGTGACT TTGGATTTCC CCAGGAGGAG	480
291 292	TTTGGCAACC AGTTCCAAAA GGCTGAAACC ATCCCTGTCC TCCATGAGAT GATCCAGCAG	540
293 294	ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGCTT GGGATGAGAC CCTCCTAGAC	600
295 296	AAATTCTACA CTGAACTCTA CCAGCAGCTG AATGACCTGG AAGCCTGTGT GATACAGGGG	660
297 298		720
299 300		780
301 302 303		840 869
303	AGIAAGGAAI GAIAACGAIC GIAACIGCA	009
305 306	(2) INFORMATION FOR SEQ ID NO: 9:	
	(2) INFORMATION FOR SEQ ID NO: 9: (i) SEQUENCE CHARACTERISTICS:	
306	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1177 base pairs	
306 307	(i) SEQUENCE CHARACTERISTICS:	
306 307 308	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1177 base pairs	
306 307 308 309	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1177 base pairs (B) TYPE: nucleic acid	
306 307 308 309 310	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1177 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both	
306 307 308 309 310 311	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1177 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both	
306 307 308 309 310 311 312 313	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1177 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: unknown	
306 307 308 309 310 311 312 313	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1177 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: unknown	
306 307 308 309 310 311 312 313 314 315	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1177 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA	
306 307 308 309 310 311 312 313 314 315 316	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1177 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS	
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306 307 308 309 310 311 312 313 314 315 316 317 318	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1177 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 286873 (D) OTHER INFORMATION: /function= "Cytokine"	
306 307 308 309 310 311 312 313 314 315 316 317 318 319 320	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1177 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 286873	
306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321	<pre>(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1177 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 286873 (D) OTHER INFORMATION: /function= "Cytokine"</pre>	
306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322	<pre>(i) SEQUENCE CHARACTERISTICS:</pre>	
306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323	<pre>(i) SEQUENCE CHARACTERISTICS:</pre>	
306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324	<pre>(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1177 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 286873 (D) OTHER INFORMATION: /function= "Cytokine"</pre>	
306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325	<pre>(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1177 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 286873 (D) OTHER INFORMATION: /function= "Cytokine"</pre>	
306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326	<pre>(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1177 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 286873 (D) OTHER INFORMATION: /function= "Cytokine"</pre>	
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306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329	<pre>(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1177 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 286873 (D) OTHER INFORMATION: /function= "Cytokine"</pre>	
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671

DATE: 06/16/94 TIME: 16:58:55

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TTG	ATTG	ATC I	AGGT	AGAG	GG G	GCGC'	rgta(C GA	GGTA.	AAGC	CCG	ATGC	CAG	CATT	CCTGAC	120
GAC	GATA	CGG 2	AGCT	GCTG	CG C	GATT	ACGT	A AA	GAAG'	TAT	TGA	AGCA'	rcc '	TCGT	CAGTAA	180
AAA	STTA	ATC :	rttt(CAAC	AG C	rgtc	ATAA	A GT	rgtc:	ACGG	CCG	AGAC'	TTA '	TAGT	CGCTTT	240
GTT:	TTTA:	TTT :	rtta <i>i</i>	ATGT	AT T	rgcT(CGAG	A GG	TTGA(GGTG	ATT'	Me	et L			294
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TCT	GCT	GGG	GCA	ATT	AGC	AGC	CCT	GCA	CTG	ACC	TTG	AGG	AGG	TAC	TTC	726
CAG	GGA	ATC	CGT	GTC	TAC	CTG	AAA	GAG	AAG	AAA	TAC	AGC	GAC	TGT	GCC	774
	GACC AAAC GTTT AST -20 AAT AST AST CYS GGG Gly 45 CTG Leu TGG Trp CTG Leu TCT Ser	GAATTGGA TTGATTGA GACGATAA AAAGTTAA GTTTTTAAA AAT ATC ASN Ile -20 AAT GCC ASN Ala AAC ACC ASN Thr TGT CTC Cys Leu 30 GGG AGC Gly Ser 45 CTG CAG Leu Gln TGG AAC Trp ASN CTG CAA Leu Gln TCT GCT Ser Ala 110	GAATTGGAGA TTGATTGATC GACGATACGG AAAGTTAATC GTTTTTATTT AAT ATC GCA Asn Ile Ala -20 AAT GCC TAT Asn Ala Tyr AAC ACC TTG Asn Thr Leu 15 TGT CTC AAG Cys Leu Lys 30 GGG AGC CAG Gly Ser Gln 45 CTG CAG CAG Leu Gln Gln TGG AAC ATG Trp Asn Met CTG CAA CAC Leu Gln His 95 TCT GCT GGG Ser Ala Gly 110	GAATTGGAGA TTATO TTGATTGATC AGGTZ GACGATACGG AGCTC AAAGTTAATC TTTTC GTTTTTATTT TTTAA AAT ATC GCA TTT ASN Ile Ala Phe -20 AAT GCC TAT GCA ASN Ala Tyr Ala AAC ACC TTG GTG ASN Thr Leu Val 15 TGT CTC AAG GAC Cys Leu Lys Asp 30 GGG AGC CAG TTG Gly Ser Gln Leu 45 CTG CAG CAG ATC Leu Gln Gln Ile TGG AAC ATG ACC Trp Asn Met Thr 80 CTG CAA CAC CTG Leu Gln His Leu 95 TCT GCT GGG GCA Ser Ala Gly Ala	GAATTGGAGA TTATCGTCA TTGATTGATC AGGTAGAGA GACGATACGG AGCTGCTGC AAAGTTAATC TTTTCAACA GTTTTTATTT TTTAATGTA AAT ATC GCA TTT CTT Asn Ile Ala Phe Leu -20 AAT GCC TAT GCA TGT Asn Ala Tyr Ala Cys 1 AAC ACC TTG GTG CTT Asn Thr Leu Val Leu 15 TGT CTC AAG GAC AGA Cys Leu Lys Asp Arg 30 GGG AGC CAG TTG CAG Gly Ser Gln Leu Gln 45 CTG CAG CAG ATC TTC Leu Gln Gln Ile Phe 65 TGG AAC ATG ACC CTC Trp Asn Met Thr Leu 80 CTG CAA CAC CTG GAG Leu Gln His Leu Glu 95 TCT GCT GGG GCA ATT Ser Ala Gly Ala Ile	GAATTGGAGA TTATCGTCAC TO TTGATTGATC AGGTAGAGGG GO GACGATACGG AGCTGCTGCG CO AAAGTTAATC TTTTCAACAG CO GTTTTTATTT TTTAATGTAT TO AAT ATC GCA TTT CTT CTT ASN Ile Ala Phe Leu Leu -20 -15 AAT GCC TAT GCA TGT GAT ASN Ala Tyr Ala Cys Asp 1 AAC ACC TTG GTG CTT CTG ASN Thr Leu Val Leu Leu 15 TGT CTC AAG GAC AGA AGA Cys Leu Lys Asp Arg Arg 30 GGG AGC CAG TTG CAG AAG Gly Ser Gln Leu Gln Lys 45 50 CTG CAG CAG ATC TTC AGC Leu Gln Gln Ile Phe Ser 65 TGG AAC ATG ACC CTC CTA Trp Asn Met Thr Leu Leu 80 CTG CAA CAC CTG GAG ACC Leu Gln His Leu Glu Thr 95 TCT GCT GGG GCA ATT AGC Ser Ala Gly Ala Ile Ser 110	GAATTGGAGA TTATCGTCAC TGCAA' TTGATTGATC AGGTAGAGGG GGCGC' GACGATACGG AGCTGCTGCG CGATTA' AAAGTTAATC TTTTCAACAG CTGTCA' GTTTTTATTT TTTAATGTAT TTGCTC' AAT ATC GCA TTT CTT CTT GCA ASN Ile Ala Phe Leu Leu Ala -20	GAATTGGAGA TTATCGTCAC TGCAATGCTC TTGATTGATC AGGTAGAGGG GGCGCTGTAG GACGATACGG AGCTGCTGCG CGATTACGTC AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTTTTATTT TTTAATGTAT TTGCTCGAGA AAT ATC GCA TTT CTT CTT GCA TCT ASN Ile Ala Phe Leu Leu Ala Ser -20 AAT GCC TAT GCA TGT GAT CTG CCT ASN Ala Tyr Ala Cys Asp Leu Pro 1 AAC ACC TTG GTG CTT CTG CAC CAA ASN Thr Leu Val Leu His Gln 15 TGT CTC AAG GAC AGA AGA GAC TCC Cys Leu Lys Asp Arg Arg Asp Phe 30 GGG AGC CAG TTG CAG AAG GCC CAT Gly Ser Gln Leu Gln Lys Ala His 45 CTG CAG CAG ATC TTC AGC CTC CTA CTG CAG CAG ATC TTC Leu Gln Gln Ile Phe Ser Leu Phe 65 TGG AAC ATG ACC CTC CTA GAC CAA Trp Asn Met Thr Leu Leu Asp Gln 80 CTG CAA CAC CTG GAG ACC TGC TTG Leu Gln His Leu Glu Thr Cys Leu 95 CTC CAA GGC GCA ATT AGC AGC CTT Ser Ala Gly Ala Ile Ser Ser Pro 110	GAATTGGAGA TTATCGTCAC TGCAATGCTT CGA TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAG GACGATACGG AGCTGCTGCG CGATTACGTA AAA AAAGTTAATC TTTTCAACAG CTGTCATAAA GT GTTTTTATTT TTTAATGTAT TTGCTCGAGA GG AAT ATC GCA TTT CTT CTT GCA TCT ATG ASN Ile Ala Phe Leu Leu Ala Ser Met -20	GAATTGGAGA TTATCGTCAC TGCAATGCTT CGCAATG TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAG GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGG AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCG GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAG ASN Ile Ala Phe Leu Leu Ala Ser Met Phe -20 -15 AAT GCC TAT GCA TGT GAT CTG CCT CAG AAC ASN Ala Tyr Ala Cys Asp Leu Pro Gln Asn 1	GAATTGGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG AAT ATC GCA TTT CTT CTT GCA TCT ATG TTC GTT ASN Ile Ala Phe Leu Leu Ala Ser Met Phe Val -20	TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC CCGGACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAAAGTTAATC TTTTCAACAG CTGTCATAAAA GTTGTCCACGG CCGGTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTT ASN Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe -20	GAATTGGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAA TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC CCGATGCC GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCAC AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGGC GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTT AC ASN ILe Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser -10 AAT ATC GCA TTT CTT CTT GCA TCT ATG TTC GTT TTT TCT ASN Ala Tyr Ala Cys Asp Leu Pro Gln Asn His Gly Leu 1 5 AAC ACC TTG GTG CTT CTG CAC CAA ATG AGG AGA ATC TCC ASN Thr Leu Val Leu His Gln Met Arg Arg Ile Ser 15 20 25 TGT CTC AAG GAC AGA AGA GAC TTC AGG TTC CCC CAG GAG Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu 30 35 70 61	GAATTGGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA CTGATGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC CCGATGCCAG GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC CAAAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA CGTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTT ATG AA Met L23 AAT ATC GCA TTT CTT CTT GCA TCT ATG TTC GTT TTT TCT ATT ASN Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser Ile -10 AAT GCC TAT GCA TGT GAT CTG CCT CAG AAC CAT GGC CTA CTT ASN Ala Tyr Ala Cys Asp Leu Pro Gln Asn His Gly Leu Leu Leu Val Leu Leu His Gln Met Arg Arg Ile Ser Pro 15 AAC ACC TTG GTG CTT CTG CAC CAA ATG AGG AGA ATC TCC CCT ASN Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser Pro 15 TGT CTC AAG GAC AGA AGA GAA GAA CTC AGG TTC CCC CAG GAG ATG Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Gln Glu Met 30 GGG AGC CAG TTG CAG AAG GCC CAT GTC ATG TCT GTC CTC CAT GLy Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu His 45 CTG CAG CAG ATC TTC AGC CTC TTC CAC ACA GAG CGC TCC TCT Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser Ser 65 CTG CAG CAG ATC CTC CTA GAC CAA CTC CAC ACT GGA CTT CAT TTP ASN Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu His 85 GCTG CAA CAC CTG GAG ACC TCC TTG CTG CAC ACT GGA CTT CAT TTP ASN Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu His 85 GCTG CAA CAC CTG GAG ACC TCC TTG CTG CAC CTG ACT GGA CTT CAT TTP ASN Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu His 85 GCTG CAA CAC CTG GAG ACC TCC TTG CTG CAC CTG ACC TTG GAG GAA CLeu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly Glu 95 CTG CTG CGG GCA ATT AGC ACC CTC TTG CTG CAC CTG ACC TTG AGG AGG CTT CAT TTG CTG CTG GGG GCA ATT AGC ACC CTG GCA CTG ACC TTG ACC CTG ACC ACC TTG ACC CTG ACC ACC GGA GAG ACC CTG CTG CTG CTG CTG CTG CTG CTG CTG C	GRATTGGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA CCAAG TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTG GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTG AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA TAGTG GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTT ATG AAA AA Met Lys Ly -23 AAT ATC GCA TTT CTT CTT GCA TCT ATG TTC GTT TTT TCT ATT GCT Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser Ile Ala -20 AAT GCC TAT GCA TGT GAT CTG CCT CAG AAC CAT GGC CTA CTT AGC Asn Ala Tyr Ala Cys Asp Leu Pro Gln Asn His Gly Leu Leu Ser 1 AAC ACC TTG GTG CTT CTG CAC CAA ATG AGG AGA ATC TCC CCT TTC Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser Pro Phe 15 TGT CTC AAG GAC AGA AGA AGA GAC TTC AGG TTC CCC CAG GAG ATG GTA Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu Met Val 30 35 CTG CAG CAG TTG CAG AAG GCC CAT GTC ATG TCT CTC CAT GAG Gly Ser Gln Leu Gln Lys Ala His Val Met Ser 50 CTG CAG CAG ATC TTC AGC CTC TTC CAC ACA GAG CGC TCC TCT GCT Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser Ser Ala 65 CTG CAA CAC CTG GAG ACC TGC TTG CTG CAC CAC ACT GGA CTT CAT CAG TTP Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu His Gln 80 CTG CAA CAC CTG GAG ACC TGC TTG CTG CAC CAC GTG GAC CTT CAT CAG TTP Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu His Gln 90 CTG CAA CAC CTG GAG ACC TGC TTG CTG CAC CAC GTG GGA CTT CAT CAG TTP Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu His Gln 90 CTG CAA CAC CTG GAG ACC TGC TTG CTG CAC CAC GTG ACC TG GGA CAC Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly Glu Gly 95 CTG CAG GAG CAC TTG AGC CTC TGC TGC CAC CTG ACC TTG AGG AGG Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly Glu Gly 105	GAATTGGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA CCAACAGCGG TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA TAGTCGCTTT GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTT ATG AAA AAG MET Lys Lys -23 AAT ATC GCA TTT CTT CTT GCA TCT ATG TTC GTT TTT TCT ATT GCT ACA Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser Ile Ala Thr -20 -15 AAT GCC TAT GCA TGT GAT CTG CCT CAG AAC CAT GGC CTA CTT AGC AGG ASN Ala Tyr Ala Cys Asp Leu Pro Gln Asn His Gly Leu Leu Ser Arg 1 AAC ACC TTG GTG CTT CTG CAC CAA ATG AGG AGA ATC TCC CCT TTC TTG ASN Thr Leu Val Leu His Gln Met Arg Arg Ile Ser Pro Phe Leu 15 20 TGT CTC AAG GAC AGA AGA AGA GAC TTC AGG TTC CCC CAG GAC ATG GTA AAA Cys Leu Lys Asp Arg Arg Asp Phe Pro Gln Gln Glu Met Val Lys 30 35 TGT CTC AAG GAC AGA AGA GCC CAT GTC ATG TCT GTC CTC CAT GAG ATG Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu His Glu Met 45 TGG CAG CAG ATC TTC AGC CTC TTC CAC ACA GAG CGC TCC TCT GCT GCT CAG CAG CAG ATC TTC AGC CTC TTC CAC CAC AGA GCG TCC TCT GCT GCC Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu His Gln Gln 80 CTG CAA CAC CTG GAG ACC TGC TTG CTG CAG GTG GAG CAA TTP ASN Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu His Gln Gln 80 CTG CAA CAC CTG GAG ACC TGC TTG CTG CAG GTG GGA GAG GAG AAA Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly Glu Gly Glu 95 TCT GCT GGG GCA ATT AGC AGC CTC TCC GCA CTG ACC TTG AGG AGG TAC TTC Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg Arg Tyr Phe

RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671

DATE: 06/16/94 TIME: 16:59:00

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389	Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe Leu Ser Thr
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401	AAGATGTTAT TTATTTTTAC TCATTTATTT ATTCTTACAT TTTATCATAT TTATACTATT 1110
403	MONICITAL TRAITITAC TCATTIATT ATTCTIACAT TTATCATAT TTATACTATT TITO
404	TATATTCTTA TATAACAAAT GTTTGCCTTT ACATTGTATT AAGATAACAA AACATGTTCA 1170
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460	(i) SEQUENCE CHARACTERISTICS:
461	(A) LENGTH: 879 base pairs
462	(B) TYPE: nucleic acid
463	(C) STRANDEDNESS: both
464	(D) TOPOLOGY: unknown
465	(ii) MOLEGIE ENDE, ADNA
466 467	(ii) MOLECULE TYPE: cDNA
468	
469	
470	(ix) FEATURE:
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487													11	11 01	DD1. D2	373.1u
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494 495	AAAGT'	FAATC	TTTT	CAAC	AG C'	rgtc.	ATAA	A GT	rgtc:	ACGG	CCG	AGAC'	TTA :	ragt(CGCTTT	240
496 497 498	GTTTT'	PATTT	TTTA	ATGT	AT T	rgct(CGAG	A GG	rtga(GGTG	ATT'	Me		AA Ai ys Ly	_	294
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504	AAT G															390
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510	Arg II	1		пец	шец	ALG	20	1.100	Ar 9	Arg	110	25	пси	FIIC	DCI	
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512	TGC T	ומ ב	ב משכ	AGA	ССТ	GAC	ттт	GGA	ттт	מממ	CAG	GAG	GAG	ттт	GGC	486
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522				65					70					75		
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524	GAT GA															630
525	Asp G	lu Th			Asp	гуѕ	Pne	_	Thr	GIU	ьeu	Tyr		GIII	ьeu	
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529	Asn As															0,0
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536	AGA A															774
537	Arg I	le Th	r Leu	Tyr	Leu	Lys	Glu	Lys	Lys	Tyr	Ser	Pro	Cys	Ala	Trp	
538	125				130					135					140	
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	INPUT SET: S2395.re	aw
540	GAG GTT GTC AGA GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC 822	
541	Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn	
542	145 150 155	
543		
544	TTG CAA GAA AGT TTA AGA AGT AAG GAA TGATAACGAT CGTAACTGCA 869	
545	Leu Gln Glu Ser Leu Arg Ser Lys Glu	
546	160 165	
547		
548	GAAGCTTAAT 879	
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SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/08/249,671

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